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OM protein - protein search, using sw model

Run on: January 3, 2002, 21:35:19 ; Search time 23.09 Seconds

(without alignments)
899.547 Million cell updates/sec

Title: US-09-497-822A-19

Perfect score: 4912

Sequence: 1 MEVOLGLGRVYPRPESKTYR.....SYQYPKILSGKVPIKFHTQ 923

Scoring table: BLOSUM62

Gapext: 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /egn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /egn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /egn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /egn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /egn2_6/ptodata/2/iaa/PCUS_CONB.pep:*

6: /egn2_6/ptodata/2/iaa/backtiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	4838.5	98.5	918	4	US-09-041-886-11	Sequence 11, Appl
2	2429	49.5	452	4	US-08-764-870-16	Sequence 16, Appl
3	2429	49.5	452	4	US-08-980-115-16	Sequence 16, Appl
4	1261	25.7	933	4	US-08-764-870-14	Sequence 14, Appl
5	1261	22.9	933	4	US-08-980-115-14	Sequence 14, Appl
6	1127	22.9	363	6	5223606-6	Patent No. 5223606
7	1078.5	22.0	984	4	US-08-764-870-15	Sequence 15, Appl
8	1078.5	22.0	984	4	US-08-980-115-15	Sequence 15, Appl
9	1065	21.7	795	1	US-07-16-82C-5	Sequence 5, Appl
10	1042	21.2	777	4	US-08-764-870-13	Sequence 13, Appl
11	1042	21.2	777	4	US-08-980-115-13	Sequence 13, Appl
12	959.5	19.5	356	6	5223606-6	Patent No. 5223606
13	795	16.2	154	4	US-09-041-886-32	Sequence 32, Appl
14	644.5	13.1	534	3	US-08-975-223-8	Sequence 8, Appl
15	644	13.1	284	2	US-08-592-244-A-24	Sequence 24, Appl
16	644	13.1	284	3	US-09-149-976-24	Sequence 24, Appl
17	636	12.9	284	3	US-08-59-188-20	Sequence 20, Appl
18	636	12.9	284	3	US-08-65-22-20	Sequence 20, Appl
19	636	12.9	284	3	US-08-55-241-20	Sequence 20, Appl
20	484.5	9.9	596	2	US-08-336-620A-16	Sequence 16, Appl
21	481	9.8	595	4	US-08-764-870-12	Sequence 12, Appl
22	481	9.8	595	4	US-08-836-620A-12	Sequence 12, Appl
23	478	9.7	591	2	US-08-336-620A-17	Sequence 17, Appl
24	478	9.7	595	4	US-09-041-886-35	Sequence 35, Appl
25	442.5	9.0	484	2	US-08-836-620A-14	Sequence 14, Appl
26	442.5	9.0	485	2	US-08-836-620A-5	Sequence 5, Appl
27	439	8.9	485	2	US-08-836-620A-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-041-886-11
; Patent 11, Application US/09041886

; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; REBIADEH, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: P-LJ 2626
; FILING DATE: 16/09/041/886 X
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8948
; INFORMATION FOR SEQ ID NO: 11;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 918 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-041-886-11

Query Match 98.5%; Score 4838.5;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 0; Mismatches 1; Indels 11; Gaps 2;
QY 1 MEVOLGLGRVYPRPSKTYRGAFQNLFOSTREVIONPGPRPEAAAPGASLLLQQQ 60
Db 1 MEVOLGLGRVYPRPSKTYRGAFQNLFOSTREVIONPGPRPEAAAPGASLLLQQQ 60

TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand
 TITLE OF INVENTION: Binding Domains
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooley Godward
 STREET: Five Palo Alto square,
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/764,870
 FILING DATE: 13-DEC-1996
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 60/008,540
 FILING DATE: 13-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Nakamura, Jack N.
 REGISTRATION NUMBER: UCAL-246/01US
 REFERENCE/DOCKET NUMBER: UCAL-246/01US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 843-5000
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 452 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: >1 linear
 MOLECULE TYPE: protein
 US-08-764-870-16

Query Match 49.5% Score 2429; DB 4; Length 452;
 Best Local Similarity 99.8%; Pred. No: 1.4e-17;
 Matches 451; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 472 GGGCGEAGAVAPGTYTRPQQLAGQESDTAPDWYPGGMVSRVPYPSPTCYKSEMPWMDSYSGP 531
 Db 1 GGGCGEAGAVAPGTYTRPQQLAGQESDTAPDWYPGGMVSRVPYPSPTCYKSEMPWMDSYSGP 531

QY 538 YGDMRLTARDHVLPIDYFPQTKCLGDAASGCHYGAUTGCSCKVFRRAEGKQY 597
 Db 533 YGDMRLTARDHVLPIDYFPQTKCLGDAASGCHYGAUTGCSCKVFRRAESQKY 592

QY 598 LCASRNDTIDKFRKNCPSCKRKCYEAGMTLQARLKLNKLQBEGEASSSTPE 657
 Db 593 LCASRNDTIDKFRKNCPSCKRKCYEAGMTLQARLKLNKLQBEGEASSSTPE 652

QY 658 ETTQKLTVSHIEGYECQPIFIYLWVLEATEPGVIVAGHDNNQDPSFAAULSSNLGEROLV 717
 Db 653 ETTQKLTVSHIEGYECQPIFIYLWVLEATEPGVIVAGHDNQDPSFAAULSSNLGEROLV 712

QY 718 HVVKWAALKPGRFLNHVDQMAWQIYSWMSGLAVFANGWRSFTVNNSRMLYFAPDLYVNEY 777
 Db 713 HVVKWAALKPGRFLNHVDQMAWQIYSWMSGLAVFANGWRSFTVNNSRMLYFAPDLYVNEY 772

QY 778 RMHRSRMSQCVRMHSQSFEGLQITPQEFLCKMKALLFLSITPVDGUKNQKFDELRMN 837
 Db 773 RMHRSRMSQCVRMHSQSFEGLQITPQEFLCKMKALLFLSITPVDGUKNQKFDELRMN 832

QY 838 YIKBLDRITACKRNPTCSRRYQIYLTQKLLDSQPIARELHOPTFDLJIKSMVSDPE 897
 Db 833 YIKBLDRITACKRNPTCSRRYQIYLTQKLLDSQPIARELHOPTFDLJIKSMVSDPE 892

QY 898 MMAELISVQPKLISGKVPIYHTQ 923
 Db 893 MMAELISVQPKLISGKVPIYHTQ 918

RESULT 2
 US-08-764-870-16
 Sequence 16, Application US/08764870
 Patent No. 6236946
 GENERAL INFORMATION:
 APPLICANT: Scanlan, Thomas S
 APPLICANT: Baxter, John D
 APPLICANT: Flitterick, Robert J
 APPLICANT: Wagner, Richard L
 APPLICANT: Kushner, Peter J
 APPLICANT: Apriletti, James W
 APPLICANT: West, Brian
 APPLICANT: DELRMYN KELDRIIACKRNPTCSRRYQIYLTQKLLDSQPIARELHOPTFDLJIKSMV
 QY 772 LVNEYRMHKSRMSQCVRMHLSQEFQWMLQITPQEFLCKMKALLFLSITPVDGUKNQKF 831
 QY 712 GEROLVHVWKWAALKPGRFLNHVDQMAWQIYSWMSGLAVFANGWRSFTVNNSRMLYFAPD 771
 Db 121 EGROKYLCA SRNDTIDKFRKNCPSCKRKCYEAGMTLQARLKLNKLQBEGEASS 180

QY 652 TTSPEETTQKLTVSHIEGYECQPIFIYLWVLEATEPGVIVAGHDNNQDPSFAAULSSNL 711
 Db 181 TTSPTEETTQKLTVSHIEGYECQPIFIYLWVLEATEPGVIVAGHDNNQDPSFAAULSSNL 240

QY 712 GEROLVHVWKWAALKPGRFLNHVDQMAWQIYSWMSGLAVFANGWRSFTVNNSRMLYFAPD 771
 Db 241 GEROLVHVWKWAALKPGRFLNHVDQMAWQIYSWMSGLAVFANGWRSFTVNNSRMLYFAPD 300

QY 832 DELRMYN KELDRIIACKRNPTCSRRYQIYLTQKLLDSQPIARELHOPTFDLJIKSMV
 QY 832 DELRMYN KELDRIIACKRNPTCSRRYQIYLTQKLLDSQPIARELHOPTFDLJIKSMV 891

RESULT 3

Sequence 16, Application US/08980115

; Patent No. 6266622
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Thomas S.
; APPLICANT: Fleiterick, Robert J.
; APPLICANT: Wagner, Richard L.
; APPLICANT: Kushner, Peter J.
; APPLICANT: West, Brian L.
; APPLICANT: Shlau, Andrew K.
; TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS
; FILE REFERENCE: UCAL-246/02US
; CURRENT APPLICATION NUMBER: US/08/980,115
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 08/764,870
; EARLIER FILING DATE: 1996-12-13
; EARLIER APPLICATION NUMBER: 60/008,606
; EARLIER FILING DATE: 1995-12-14
; EARLIER APPLICATION NUMBER: 60/008,543
; EARLIER FILING DATE: 1995-12-13
; EARLIER APPLICATION NUMBER: 60/008,540
; EARLIER FILING DATE: 1995-12-13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 16
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (184)-(437)
; OTHER INFORMATION: minimal ligand binding domain

US-08-980-115-16

Query Match 49.5%; Score 2429; DB 4; Length 452;
Best Local Similarity 99.8%; Pred. No. 1,4e-171;
Matches 451; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query 472 GGGGAGAYAPGYTTRPPOGLAOESDFTAPDWPYPGGMVSRVPYPSPTCVKSENGPWW 531
Db 1 GGGGAGAYAPGYTTRPQGLAQSDETAQDWYPGMVSRVPYPSPTCVKSENGPWW 60
Query 532 DSYSGPYGDMRLETARDHVLPIDYFPPQTKCLICGDEASGHYGAUTGCSCKVFKRAA 591
Db 61 DSYSGPYGDMRLETARDHVLPIDYFPPQTKCLICGDKASGHYGAUTGCSCKVFKRAA 120
Query 592 EGKOKYLCAQRNDCTIDKFRKNCPSCLRKYCAGMTLGARKLKLGNLKQEGEREASS 651
Db 121 EGKOKYLCAQRNDCTIDKFRKNCPSCLRKYCAGMTLGARKLKLGNLKQEGEREASS 180
Query 652 TTSPIBETMQLTVSHIEGYCOPJFLNVAEPEGYVCAGHDNNQPSDFAAALLSSNEL 711
Db 181 TTSPIBETMQLTVSHIEGYCOPJFLNVAEPEGYVCAGHDNNQPSDFAAALLSSNEL 240
Query 712 GERQLVHVVVKWAKALPGLPFRNLHYDDOMAVIOTSNWGMGLMFANGWRSFTNYNSMLYFAPD 771
Db 241 GERQLVHVVVKWAKALPGLPFRNLHYDDQMAVIOTSNWGMGLMFANGWRSFTNYNSMLYFAPD 300
Query 772 LVNEYRMKSRMYSOCYVRMHSQEQFWLQTPOQFLCMKALLLESTIPVDGLKNQKF 831
Db 301 LVNEYRMKSRMYSOCYVRMHSQEQFWLQTPOQFLCMKALLLESTIPVDGLKNQKF 360

Query Match 25.7%; Score 1261; DB 4; Length 933;
Best Local Similarity 34.1%; Pred. No. 6.9e-18;
Matches 346; Conservative 128; Mismatches 318; Indels 224; Gaps 34;

Query 38 GPRHPEAASAAP-----
Db 8 GPRAPHVAGGPPSPVEVGSPPLCRPAAGPFGSQTSDTLPVEVAIPSIDGLLFPRPCQGQ 67

Db 482 APGASCLLPRDGLPSTSASAAGA-APALY -PALGLNG -----LPQI.GYQAAVLE 532
 Qy 515 -VPPSPPTCVKSEMGPMWIDSYSPGYGDMRILEFARDHVLPTDYYFP--POKTCILICDEAS 571
 Db 533 GLPVQVPPYL-NYLRPDSEASQP-----QYSFESELPOKTCILICDEAS 575
 Qy 572 GCHYGAATCGSKCKVEFKRAEGKOKYLCASRNDCDTDKFRKNCPSCLRKYEAGMTLIG 631
 Db 576 GCHYGVLRGSKCKVEFKRAEMEHOHNYCAGRNDCTVDKTRKNCPCRLKCQAGMVG 635
 Qy 632 ARKKLGNLKLQEEGASSTSP-----TEPIOTKLVSHIEGECQFCPLFLNLEATE 685
 Db 636 GRKEKKENKVRYVRALDAVALQPLGPYNESOALSORFTESPQDQLIPPLNLMSIE 695
 Qy 686 PGVVAUGHDNQNPDSFAALLSSLNELGEROLVHVVKWAKALPGRFLHVDQMAVQYSW 745
 Db 696 PDVIYAGHDNTNPDTSSSLTTSNQERQLLSVVEWSKS1PGRFLHLDDQTUQYSW 755
 Qy 746 MGLMVFMANGWRSFTNVSRMFLYAPDLYNEYRMHKSRMYSQCVRMHLSQEFGMQLITP 805
 Db 756 MSLMVFGLGWRSKHKVSGQMLYAPDLYNLRNQRMKESSEFSCLUTMWQ1PQEYKQLQSQ 815
 Qy 806 QEFFLCKMKALLLTSIIPVGDLMQKFDELRMNVIKBLDRJAKRNPTCSRRYEQYLTK 865
 Db 816 EPEFLCKMRVLLNTIPLEGLRSQTOEFEMRSYIRELIKAGLQRKGVYSSSQRFYQLTK 875
 Qy 866 LLDSVQPIAREHQFTPDLLKISHMVSDFPEMMAIIISVQPKLISGKVKPYIYH 921
 Db 876 LLDNLHDLVKQHLYCLNTFIQSRLALSVEPFEMMSEVIARQPKLAGMVKPLFH 931

RESULT 6
 5223606-6
 ; Patent No. 5223606
 ; APPLICANT: BLAUDIN DE THE, HUGHES; MARCHIO, AGNES; TIOLLAIS,
 ; PIERRE; DEJAN, ANNE
 ; TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED
 ; PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA
 ; NUMBER OF SEQUENCES: 11
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/134,130
 ; FILING DATE: 17-DEC-1987
 ; PRIOR APPLICATION DATA:
 ; SEQ ID NO: 16:
 ; LENGTH: 363
 5223606-6

Query Match 22.9% Score 1127; DB 6; Length 363;
 Best Local Similarity 56.0%; Pred. No. 1.5e-75; Mismatches 72; Gaps 1;

Db 1 CLICDEASCHYGAUTCSCKVFKRAEGKOKYLCASRNDCDTDKFRKNCPSCLRK 622
 Qy 623 CYEAGMTLGARKLKLGNLQEEGAEASSSTSP- -ETTOKLTVSHIEGECQFCPLNV 680
 Db 61 CCQAGMVLGGRKTFKKENKVYRMALDAVALPAVGIPNEQRRTFSQEIQLIPPLNL 120
 Qy 681 LEATEPGVYCAHHDNQNPDSFAALLSSLNELGERQLYHVVKWAALKALGCFRNLHVDDOMAV 740
 Db 121 LMSIEPDVIYAGHDNTKPDTSSSLTSNLQGRQLLSVVKWSLPGFRNLHDDQITL 180

Qy 741 IQYSRMGMLVNEAGWRSFTNVNSRMLYAPDLYFNEYRMHKSMSYSCVURHLSQEFGW 800
 Db 181 IQYSRMWSLNAVGWRSKHKVQSMOLYAPDULTRMKEQFQFVSYSLCLTMWQ1PQEFV 240
 Qy 801 LQTPQEFQFCMKALLLTSIIPVGDLMQKFDELRMNVIKBLDRJAKRNPTCSRRF 860
 Db 241 LQSQEEFLCMKVLLNTIPLEGLRSOSOEFMRSSYIRELIKAGLQRQGVSSQRF 300
 Qy 861 YQLTKLDSVQPARELHQFTFDLIRSHMYSVDFPEMMAIIISVQPKLISGKVKPYIYF 927

Db 301 YQLTKLDSVQPARELHQFTFDLIRSHMYSVDFPEMMAIIISVQPKLISGKVKPYIYF 360
 Qy 921 H 921
 Db 361 H 361

RESULT 7
 US-08-764-870-15
 ; Sequence 15, Application US/08/64870
 ; Patent No. 6236946
 ; GENERAL INFORMATION:
 ; APPLICANT: Scanlan, Thomas S
 ; APPLICANT: Baxter, John D
 ; APPLICANT: Fletterick, Robert J
 ; APPLICANT: Wagner, Richard L
 ; APPLICANT: Kushner, Peter J
 ; APPLICANT: Aperleit, James W
 ; APPLICANT: West, Brian
 ; TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand
 ; TITTLE OF INVENTION: Binding Domains
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooley Godward
 ; STREET: Five Palo Alto Square,
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/764,870
 ; FILING DATE: 13-DEC-1996
 ; CLASSIFICATION: 530
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/008,540
 ; FILING DATE: 13-DEC-1995
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/008,543
 ; FILING DATE: 13-DEC-1995
 ; PRIORITY APPLICATION DATA: 606
 ; APPLICATION NUMBER: US 60/008,606
 ; FILING DATE: 14-DEC-1995
 ; ATTORNEY/AGENT INFORMATION: X
 ; NAME: Nakamura, Jackie N
 ; REGISTRATION NUMBER: 35-966
 ; REFERENCE/DOCKET NUMBER: UCAL-246/01US
 ; TELECOMMUNICATION: (650)843-5000
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 984 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-764-870-15

Query Match 22.0% Score 1078.5; DB 4; Length 984;
 Best Local Similarity 32.0%; Pred. No. 2.2e-71;
 Matches 300; Conservative 101; Mismatches 254; Indels 259; Gaps 30;

Qy 98 SPOAHRRGPGYGL-----VLDDEQQP-SQPSALECHPERGCVPEP ---GAIAASK 145
 Db 238 SPNAEURNGRSSHSPAHASNVGSPLSSPLSSMKSSSSPNSHCSYKSPYSSPNVTLSRV 297

Qy 146 GLPQQL-----PAPPDEDD----SAAPSTL-SLLGP-----TPGGLSSCSADIKD 185

QY 668 TEGWECQPLFLAVNLEATEPGVVCAGHDNNQPDSSAFLSSLNLGEGLFRQLVHVVKNAKALP 727
 Db 733 ---ALTSPVMLENIEPEITVAGYDSSKPDTAENILSTUNLAGKQMQVVKAKVLP 788
 QY 728 GFRNLHVDQMAVTQYSWMGLMVEAMGWSRFVNNSRMLYFAPDLYFNEYRMHKSRYMSQ 787
 Db 789 GFKNLPLEDQTLLQISWMCLSSFAULSWRSYKHTNQFLYFAPDLYFNEYRMHKSRYMSQ 848
 QY 788 CYVRMRLHSQEFGWQLOQTPOEFICMKALLFSTIYDGLKNOKFDELMTYIKESTRILIA 847
 Db 849 CQGMHQISLQFVRQLTFFEEXTIMKVILLISTIPDGKLSQAFAEMTRNYIKELRKMYT 908
 QY 848 CRKRNPTSCSRFYOLTKILLSVQPAARELHOFTFDLILKSHMVSDFPFRMAETISYQV 907
 Db 909 KCPNNSGOSWQRFYOLTKLQDSMHDLVSLDLEFCYTFRRESHALKVFPMVLEISDQL 968
 QY 908 PKILSGKVVKPIYFH 921
 Db 969 PKVESGNAKPLYFH 982

RESULT 9
 US-07-716-827C-5
 ; Sequence 5, Application US/07716827C
 ; Patent No. 5125916

; GENERAL INFORMATION:
 ; APPLICANT: Simons Jr., Stoney S.
 ; APPLICANT: Yamamoto, K. R.
 ; APPLICANT: Chakraborti, P. K.
 ; APPLICANT: Garabedian, M. J.
 ; TITLE OF INVENTION: SUPER GLUCOCORTICOID RECEPTORS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Cushman, Darby & Cushman
 ; STREET: Eleventh floor, 1615 L Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20036-5601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/VMS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATE: 07/16, 827C
 APPLICATION NUMBER: US/07/16, 827C
 FILING DATE: 1991/06/19
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Scott, Watson T.
 REGISTRATION NUMBER: 26, 581

REFERENCE/DOCKET NUMBER: WTS/5683/84453
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)82613000
 TELEX: (202)822-8944

INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 795 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear

US-07-716-827C-5

Query Match Score 1065; DB 1; Length 795;
 Best Local Similarity 32.0%; Pre. No. 1.6e-70; Gaps
 Matches 314; Conservative 110; Mismatches 268; Indels 288; Gaps

Qy 20 RGAFQNLFOQSVR---EVIONQGPBRHPEAASAAPPGASLLL-----OQQQQQQQQQ 68
 Db 24 RGSMDFYKSLRGATKVASSSPVAAASQADSQKQRTLDFSKGSTSNVQRQQQQQ 83

Qy 69 QQQQQQQQQQQQQQETSD-----ROQQQQQED-GSPQAHR----RGPTGYLYI 112

Db	84	QQQQQQQQQQQQQQQQPGLSKAVSLSMGLYMGETETKVMNDLGYPQQQLGSSGEDFRLL 143
Qy	113	DE----EQQPSOPSALECHPERSCVPEPGAAYAASKGLPQQLPQLAPPDDEDSAAPSTLS 167
Db	144	EESIUNLNRSSTSVPENPKSSTSATGC-----
Qy	168	LLGPPFPGLSSCSDLDKILSEASTMOLLOOOOFAVESEGSSGRAREASGAPTSKDNY 227
Db	177	----FPKTH----SDASS----SVKLJ 205
Qy	228	LGGTTSIDNAKELGKAVSYMSMGLGVEALEHLSPEQUELRDCMYPPLGVPPAVRPTPC 287
Db	206	PTDQSTF----DLIKDLEFSAG----SPKDNTNESPWRSDSL----IDENLJS 246
Qy	288	PLA-----ECKGSLLDDSAG--KSTPDTAAEYSP-----FKGG 317
Db	247	PLAGDDDPFILEGNINEDCRKPLIPDTKIKDGTTLSSPSSVALPYKTERDNDFTIEL 306
Qy	318	YTKG-LEGESLG---CSGAAAGSSGTLPLSTS-----LYKSGA-----LDDEAAY 361
Db	307	CTPGVIKOKLPGVYCO---ASPGTNLIGNKMSAISVHGVSNTSGGQMYHYDMNTASLS 362
Qy	362	QSRWYNNFPIALAPPPPPLPHARIKNLNLDYGSWAAAAACQRYCDLASHLGAGA 421
Db	363	QQDD---QKVFNVAPIPIP-----VGSEN-----W-----NRCQ----- 388
Qy	422	AGPGSSGPSAAASSSWHTLTFTAEGQLYPCGGGGGGGGGGGGGGGEAGAV 481
Db	389	--GSGEBDSLTSI-----GALNFP----- 408
Qy	482	APCYTRPQGLAGOESDFTAPDWYPGGMVRVYPYPSPTCVKSEMGFWMDSYSGPGDM 541
Db	409	FSNGYSSP----GMRPDVSSP-----PS-----SSSATG-- 434
Qy	542	RLETARDHVLPDYYFPQKTCUCLICGDEASGCHYGAITCGSCRVFKRAEGQKYLCAS 601
Db	435	-----PPPKLCLVCSDAESGCHYGLTCGSKCFVKRAVEGHHNLYCAG 478
Qy	602	RNDCTIDKFRRKNCPSCLRKCYEAGMTLGARKLKJUGNLKQEEGEASSTSPTTEETQ 661
Db	479	RNDCTIDKFRRKNCPSCLRKCYRKCLQGMNLEARKTK----KKGQIQTAGTQSQTDSNP 534
Qy	662	KLTIVSHIGEYCOPFLNVAEATPGVYCAHGDNQPSFAALLSLSNELGERQYHVK 721
Db	535	NKTTIVPAALPQPTPLSLLVEPEPLYAGDSSVPDSAWRIMTUNMLGGROVIAVK 594
Qy	722	WAKALPGERFLHVDQMAVIOYSWMGLMVFAMGWRSFTNVNSRMLKFADLVNEYRMHK 781
Db	595	WAKAIGLIRNLHDDQMTLQYSWMFMAFLGWRSFTROSSNLLCAPDLINEORMSL 654
Qy	782	SRMYSOCVYMRHLSQEFGWLQITPOECMKAIIIFSLIPVDGKLQKFFDELRYMIKE 841
Db	655	POMYDQCKHMLFVSSSLQRQSYSEYLCMKTLLSSVPPGKLOSEEFDTRMYYIKE 714
Qy	842	LDRILACKRKNPNTSCSRFYQLTKLSDVQPIAREHQFTDILLISHMVSVDPEMMAE 901
Db	715	LGKAIYKREGNSQNWFYOTKLIDSMHEVNUILTYCFQTFELKTM-STIEFPMLAE 773
Qy	902	1ISVQYKPLISGKVKPYFH 921
Db	774	ITTNQEKYSNNNTKULIHF 793

RESULT 10
S-08-764-870-13
Sequence 13, Application US/08764870
Patent No. 6236946
GENERAL INFORMATION:
APPLICANT: Scanlan, Thomas S
APPLICANT: Baxter, John D
APPLICANT: Fetterick, Robert J
APPLICANT: Veltman, Edward C

APPLICANT: Kushner, Peter J
 APPLICANT: Aprilletti, James W
 APPLICANT: West, Brian
 TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand Binding Domains
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooley Godward
 STREET: Five Palo Alto square, 3000 El Camino Real
 CITY: Palo Alto
 STATE: CA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/764,870
 FILING DATE: 13-DEC-1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/008,540
 FILING DATE: 13-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/008,543
 FILING DATE: 13-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/008,606
 FILING DATE: 14-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Nakamura, Jack TEE N
 REGISTRATION NUMBER: 35,966
 REFERENCE/DOCKET NUMBER: UCAL-246/01US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650)184-35000
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 777 amino acids
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-764-870-13

Query Match 21.2% Score 1042; DB 4; Length 777;
 Best Local Similarity 32.6%; Pred No. 8e-69; Mismatches 95; Indels 266; Gaps 31;

Matches 298; Conservative 153

QY 121 POSALECHPERGVCP-----PGAVAAASKGLPQLPA-----
 DB 15 PSSVLA-QERQDVDFYKTLRGGATVKVSASSPASLAVSQSDSKQRRLVDFPRGSVSN 72

QY 154 -PPDEDDSAAPSTLSLGP-----FP----GLSSCSADLKDLSEASTMQLL 196
 DB 73 AQOPDLSKAVSISLGMGLYMGTEKYMGNDLGFPOQQISLSSGETDLK - LLEESIANL- 129

QY 197 QQQQEAVSEGGSSGRAEASGPT-----SSKDNYL-GTGSTTSIDNAK----- 239

DB 130 -NRSTSVPEPKSSASTAVSAAPTEKEFKTHSDVSSEQHLKGQTGNGNVKLYTD 187

QY 240 ---ELCKAVSYSMGLGVEAELHSLSGEOL-----RGD-----CNYAPILGVPPAVRPT 284

DB 188 QSTDILQDLESMSG-----SPGKEINESPWSDLIDENCLLSPPAGE----- 231

QY 285 PCAPLAEKGSLLDDS---AGKSTEDTAEYSPFKGGYTKLEGESLGCGSSAAGSSGTL 341

DB 232 -----DDSTPLLEGNSNED-----CK -----PL 248

QY 342 ELPSTLSLYKS GALDEAAYQS RDYNNFPLLAGRPPPPP PHARIKLENPLDGSW 401

RESULT 11
 US-08-980-115-13
 Sequence 13, Application US/08980115
 ; Patent No. 6266622
 ; GENERAL INFORMATION:
 ; APPLICANT: Scanlan, Thomas S.
 ; APPLICANT: Baxter, John D.
 ; APPLICANT: Flitterick, Robert J.
 ; APPLICANT: Wagner, Richard L.
 ; APPLICANT: Kushner, Peter J.
 ; APPLICANT: Aprilletti, James W.
 ; APPLICANT: West, Brian L.
 ; APPLICANT: Shlau, Andrew K.
 ; TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS
 ; FILE REFERENCE: UCAL 246/02US
 ; CURRENT APPLICATION NUMBER: US/08/980,115
 ; CURRENT FILING DATE: 1997-11-26
 ; EARLIER APPLICATION NUMBER: 08/764,870
 ; EARLIER FILING DATE: 1996-12-13
 ; EARLIER APPLICATION NUMBER: 60/008,606
 ; EARLIER FILING DATE: 1995-12-14
 ; EARLIER APPLICATION NUMBER: 60/008,543
 ; EARLIER FILING DATE: 1995-12-15
 ; EARLIER APPLICATION NUMBER: 60/008,540
 ; EARLIER FILING DATE: 1995-12-13
 ; NUMBER OF SEQ ID NO: 17
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 13
 ; LENGTH: 777
 ; TYPE: PRT

ORGANISM: Homo sapiens
 FEATURE: DOMAIN
 NAME/KEY: DOMAIN
 LOCATION: (506)..(762)
 OTHER INFORMATION: minimal ligand binding domain
 US-08-980-115-13

RESULT 12

Query Match 21.2%; Score 1042; DB 4; Length 777;
 Best Local Similarity 32.6%; Pred. No. 8e-69; Mismatches 95; Indels 266; Gaps 31;

Matches 298; Conservative 95; Mismatches 255; Indels 266; Gaps 31;

Db 121 POSALCHPERGCVPE-----PGAVAASKGKLPQLPA----- 153
 Qy 15 PSVSLA-QERGVNDFYKTLRGGATVKYSASSPLAVASQDSKQRRLVDPKGYSVN 72

Db 154 -PPDDDSAMPSTLSSLGP-----FP-----GLSSCSADLKDLSPASTMOLL 196
 Qy 73 AQPDLSKAYSLSMGLYMGETETKWMGNDLGPQOISLUSGETDLK--LLIESIANL- 129

Db 197 QQQQEAVSEGGSSGRARESGAPT-----SSKDNYL-GCTTISDAK----- 239

Db 130 -NRSTSVPNPKSSAATVSAAPTEKEFPTKTHSDVSQQHQHKGQTGTNGGNVLYTTD 187

Qy 240 ---ELCKAIVSMGLGVEALEHLSPEQL---RGD----CNYAPLGLGPPAVPPT 284
 Db 188 QSTFDIQLDIEFSSG-----SPGKETNEPWRSIDLIDENCLLSPAGE----- 231

Qy 285 PCAPLAECKSLLDDS---AGKSTDDTAEYSPFKGGTYKGLEGSLGSGCSAAAGSSGTL 341
 Qy 232 -----DSFSLLEGNSNED-----CK-----PL 248

Qy 342 ELPSTLSLYKSGALDEAAAYQSRYYNFPLALAGGPPPPPHPHARIKLENPDYGSAW 4.01
 Db 249 ILPDTPKPKID-----NGDLVSSPSNTLP-----QVTKTEKDFIELCT 288

Qy 402 AAAAQCRYDL---ASLRGAGAAGPGSCSPSAASSSHHTLTAAECOLYGICGGGG 4.58
 Db 289 PGVIQEKLUTVYCAQSPLNLIG-----NKMAISVHGYSTS----- 327

Qy 459 GGGGGGGGGGGGGGEAVAPYGYTRPQOGLAGOBESDFAPDV-----W----- 506
 Db 328 -----GGQM---YHMNTNTASLSSQODQKKTFNVPIPVGSEWWNR 366

Qy 507 -----YPGGMVSRVYPSPCTYKSEMGMFWMDSYSSGPYGDMLRETDHV 550
 Db 367 CQGSDDDNLTSLGTLNFPRTVFSNGYSSPS-----MRP-----DVSSPPSSSTATG 4.15

Qy 551 LPIDYFPPDKTCLIGDEASCGHYGALTGCSCKVFERRAECKQKYLCAASRDCTIDKF 610
 Db 416 -----PPKPLCLVCSDEASGCHHYGVLTCGSKCKVFERRAECKQKYLCAASRDCTIDKF 468

Qy 611 RRKNCPSCRKCYEAGMTLGLARKLKLGNLKGEEBASSTSPTEETTO--KLTVSH 667
 Db 469 RRKNCPACRYKQLPQITPFLCKMLKLNQKFEDLRRNMYKELDRIA 847

Qy 668 IEGYECQPIFLNLEIAEPGVYCAGHDNNQNPDSFAALLSSNLFGEROLHVYKWAALP 727
 Db 523 ATLPOLPTPLVSLLEVIEPVLYAGDSSVPDSTWRIMTTLNLLGGROVIAAKWAKAIP 582

Qy 728 GFRNHLYDDOMAVIYQYSWNGLMYFAMGWSRFIWNSRMLYFADLVENEYRMHKSRSYQ 787
 Db 583 GFRNHLYDDQMTLQYQSYWMLFAMGWSRSYQSSANILCFADPLLINEQRMLPCMYDQ 642

Qy 788 CVMRPHLSQPFQGWQIOTPFLCKMLKLNQKFEDLRRNMYKELDRIA 847
 Db 643 CKHMLYVSSHLRQVSFEYLCKMTLILLSSPKDGKLSQEFDERMVYKELGAIV 702

Qy 848 CKRKNPCTCSRRFYQTLKLDSTQPIARELHFTFDLLIKSHMSVDFPEMMAEISVQ 907
 Db 703 KREGNQSNQWQRFQYQTLKLDSSHEVVENLNQCFQTFDLKTM-SIEFPPEMMAEITNQI 761

Db 762 PKYSNGNIKLLFH 775

RESULT 13

Query Match 19.5%; Score 959.5; DB 6; Length 356;
 Best Local Similarity 52.1%; Pred. No. 3.4e-63;
 Matches 189; Conservative 62; Mismatches 99; Indels 13; Gaps 6;

Qy 563 CLICGDEASGCHYGAATCGSCKVFEKRAEKGQKYLCAASRDCTIDFKRKNCPCSRIRK 622
 Db 1 CLVCSDEASGCHYGVLTGCSCKVFEKRAEKGQHNYLCAGRNDCTIDKIRRKNCPCRYRK 60

Qy 623 CTEAGMFLGARKLKLQKLNQKQEGEASSSTSPEETTO--KLTVSHTEYECOPITM 679
 Db 61 CLOAGMNLEARTKK-----KIKGQIQTATGVSQETSENPGNKTIVPAPLQLPTPLV 114

Qy 680 VLEAIEPGVYCAGHDNNQNPDSFAALLSSNLFGEROLHVYKWAALPGRNLHYDDQA 739
 Db 115 LLEVTEPEVLTAGTDSVPDSTWRIMTTLNLLGGROVIAAVKWAAPGPNLHLDQNT 174

Qy 740 VIOYSWNGLMYFAMGWSRFIWNSRMLYFADLVENEYRMHKSRSYQSCVYMRHLSQEFQ 799
 Db 175 LLQYSWMLFLMA ALGWSYRSQSSANILCFADPLLINEQRMLPCMYDQCKHMLYVSELH 233

Qy 800 WLIQTPDFFLCKMLLFLSTIPVDGLKLNQKFEDLRRNMYKELDRIAKRNPPSCS-R 858
 Db 234 RQVSYEEYLCMKYLLSVPKDGKLSQEFDERMVYKELGAIV KREGLESSONWQ 292

Qy 859 REYQLTKLDSVQPIARELHFTFDLLIKSHMSVDFPEMMAEITSVQPKLTSQVVKVPT 918
 Db 293 RFYQLTKLDSRHEVVENLNQCFQTFDLKTM-SIEFPPEMMAEITNQIYTSNGNIKIL 351

Db 352 LFH 354

RESULT 14

Query Match 19.5%; Score 959.5; DB 6; Length 356;
 Best Local Similarity 52.1%; Pred. No. 3.4e-63;
 Matches 189; Conservative 62; Mismatches 99; Indels 13; Gaps 6;

Qy 563 CLICGDEASGCHYGAATCGSCKVFEKRAEKGQKYLCAASRDCTIDFK 622
 Db 1 CLVCSDEASGCHYGVLTGCSCKVFEKRAEKGQHNYLCAGRNDCTIDKIRRKNCPCRYRK 60

Qy 623 CTEAGMFLGARKLKLQKLNQKQEGEASSSTSPEETTO--KLTVSHTEYECOPITM 679
 Db 61 CLOAGMNLEARTKK-----KIKGQIQTATGVSQETSENPGNKTIVPAPLQLPTPLV 114

Qy 680 VLEAIEPGVYCAGHDNNQNPDSFAALLSSNLFGEROLHVYKWAALPGRNLHYDDQA 739
 Db 115 LLEVTEPEVLTAGTDSVPDSTWRIMTTLNLLGGROVIAAVKWAAPGPNLHLDQNT 174

Qy 740 VIOYSWNGLMYFAMGWSRFIWNSRMLYFADLVENEYRMHKSRSYQSCVYMRHLSQEFQ 799
 Db 175 LLQYSWMLFLMA ALGWSYRSQSSANILCFADPLLINEQRMLPCMYDQCKHMLYVSELH 233

Qy 800 WLIQTPDFFLCKMLLFLSTIPVDGLKLNQKFEDLRRNMYKELDRIAKRNPPSCS-R 858
 Db 234 RQVSYEEYLCMKYLLSVPKDGKLSQEFDERMVYKELGAIV KREGLESSONWQ 292

Qy 859 REYQLTKLDSVQPIARELHFTFDLLIKSHMSVDFPEMMAEITSVQPKLTSQVVKVPT 918
 Db 293 RFYQLTKLDSRHEVVENLNQCFQTFDLKTM-SIEFPPEMMAEITNQIYTSNGNIKIL 351

Db 352 LFH 354

RESULT 15

Query Match 19.5%; Score 959.5; DB 6; Length 356;
 Best Local Similarity 52.1%; Pred. No. 3.4e-63;
 Matches 189; Conservative 62; Mismatches 99; Indels 13; Gaps 6;

Qy 563 CLICGDEASGCHYGAATCGSCKVFEKRAEKGQKYLCAASRDCTIDFK 622
 Db 1 CLVCSDEASGCHYGVLTGCSCKVFEKRAEKGQHNYLCAGRNDCTIDKIRRKNCPCRYRK 60

Qy 623 CTEAGMFLGARKLKLQKLNQKQEGEASSSTSPEETTO--KLTVSHTEYECOPITM 679
 Db 61 CLOAGMNLEARTKK-----KIKGQIQTATGVSQETSENPGNKTIVPAPLQLPTPLV 114

Qy 680 VLEAIEPGVYCAGHDNNQNPDSFAALLSSNLFGEROLHVYKWAALPGRNLHYDDQA 739
 Db 115 LLEVTEPEVLTAGTDSVPDSTWRIMTTLNLLGGROVIAAVKWAAPGPNLHLDQNT 174

Qy 740 VIOYSWNGLMYFAMGWSRFIWNSRMLYFADLVENEYRMHKSRSYQSCVYMRHLSQEFQ 799
 Db 175 LLQYSWMLFLMA ALGWSYRSQSSANILCFADPLLINEQRMLPCMYDQCKHMLYVSELH 233

Qy 800 WLIQTPDFFLCKMLLFLSTIPVDGLKLNQKFEDLRRNMYKELDRIAKRNPPSCS-R 858
 Db 234 RQVSYEEYLCMKYLLSVPKDGKLSQEFDERMVYKELGAIV KREGLESSONWQ 292

Qy 859 REYQLTKLDSVQPIARELHFTFDLLIKSHMSVDFPEMMAEITSVQPKLTSQVVKVPT 918
 Db 293 RFYQLTKLDSRHEVVENLNQCFQTFDLKTM-SIEFPPEMMAEITNQIYTSNGNIKIL 351

Db 352 LFH 354

RESULT 16

Query Match 19.5%; Score 959.5; DB 6; Length 356;
 Best Local Similarity 52.1%; Pred. No. 3.4e-63;
 Matches 189; Conservative 62; Mismatches 99; Indels 13; Gaps 6;

Qy 563 CLICGDEASGCHYGAATCGSCKVFEKRAEKGQKYLCAASRDCTIDFK 622
 Db 1 CLVCSDEASGCHYGVLTGCSCKVFEKRAEKGQHNYLCAGRNDCTIDKIRRKNCPCRYRK 60

Qy 623 CTEAGMFLGARKLKLQKLNQKQEGEASSSTSPEETTO--KLTVSHTEYECOPITM 679
 Db 61 CLOAGMNLEARTKK-----KIKGQIQTATGVSQETSENPGNKTIVPAPLQLPTPLV 114

Qy 680 VLEAIEPGVYCAGHDNNQNPDSFAALLSSNLFGEROLHVYKWAALPGRNLHYDDQA 739
 Db 115 LLEVTEPEVLTAGTDSVPDSTWRIMTTLNLLGGROVIAAVKWAAPGPNLHLDQNT 174

Qy 740 VIOYSWNGLMYFAMGWSRFIWNSRMLYFADLVENEYRMHKSRSYQSCVYMRHLSQEFQ 799
 Db 175 LLQYSWMLFLMA ALGWSYRSQSSANILCFADPLLINEQRMLPCMYDQCKHMLYVSELH 233

Qy 800 WLIQTPDFFLCKMLLFLSTIPVDGLKLNQKFEDLRRNMYKELDRIAKRNPPSCS-R 858
 Db 234 RQVSYEEYLCMKYLLSVPKDGKLSQEFDERMVYKELGAIV KREGLESSONWQ 292

Qy 859 REYQLTKLDSVQPIARELHFTFDLLIKSHMSVDFPEMMAEITSVQPKLTSQVVKVPT 918
 Db 293 RFYQLTKLDSRHEVVENLNQCFQTFDLKTM-SIEFPPEMMAEITNQIYTSNGNIKIL 351

Db 352 LFH 354

RESULT 17

Query Match 19.5%; Score 959.5; DB 6; Length 356;
 Best Local Similarity 52.1%; Pred. No. 3.4e-63;
 Matches 189; Conservative 62; Mismatches 99; Indels 13; Gaps 6;

Qy 563 CLICGDEASGCHYGAATCGSCKVFEKRAEKGQKYLCAASRDCTIDFK 622
 Db 1 CLVCSDEASGCHYGVLTGCSCKVFEKRAEKGQHNYLCAGRNDCTIDKIRRKNCPCRYRK 60

Qy 623 CTEAGMFLGARKLKLQKLNQKQEGEASSSTSPEETTO--KLTVSHTEYECOPITM 679
 Db 61 CLOAGMNLEARTKK-----KIKGQIQTATGVSQETSENPGNKTIVPAPLQLPTPLV 114

Qy 680 VLEAIEPGVYCAGHDNNQNPDSFAALLSSNLFGEROLHVYKWAALPGRNLHYDDQA 739
 Db 115 LLEVTEPEVLTAGTDSVPDSTWRIMTTLNLLGGROVIAAVKWAAPGPNLHLDQNT 174

Qy 740 VIOYSWNGLMYFAMGWSRFIWNSRMLYFADLVENEYRMHKSRSYQSCVYMRHLSQEFQ 799
 Db 175 LLQYSWMLFLMA ALGWSYRSQSSANILCFADPLLINEQRMLPCMYDQCKHMLYVSELH 233

Qy 800 WLIQTPDFFLCKMLLFLSTIPVDGLKLNQKFEDLRRNMYKELDRIAKRNPPSCS-R 858
 Db 234 RQVSYEEYLCMKYLLSVPKDGKLSQEFDERMVYKELGAIV KREGLESSONWQ 292

Qy 859 REYQLTKLDSVQPIARELHFTFDLLIKSHMSVDFPEMMAEITSVQPKLTSQVVKVPT 918
 Db 293 RFYQLTKLDSRHEVVENLNQCFQTFDLKTM-SIEFPPEMMAEITNQIYTSNGNIKIL 351

Db 352 LFH 354

RESULT 18

Query Match 19.5%; Score 959.5; DB 6; Length 356;
 Best Local Similarity 52.1%; Pred. No. 3.4e-63;
 Matches 189; Conservative 62; Mismatches 99; Indels 13; Gaps 6;

Qy 563 CLICGDEASGCHYGAATCGSCKVFEKRAEKGQKYLCAASRDCTIDFK 622
 Db 1 CLVCSDEASGCHYGVLTGCSCKVFEKRAEKGQHNYLCAGRNDCTIDKIRRKNCPCRYRK 60

Qy 623 CTEAGMFLGARKLKLQKLNQKQEGEASSSTSPEETTO--KLTVSHTEYECOPITM 679
 Db 61 CLOAGMNLEARTKK-----KIKGQIQTATGVSQETSENPGNKTIVPAPLQLPTPLV 114

Qy 680 VLEAIEPGVYCAGHDNNQNPDSFAALLSSNLFGEROLHVYKWAALPGRNLHYDDQA 739
 Db 115 LLEVTEPEVLTAGTDSVPDSTWRIMTTLNLLGGROVIAAVKWAAPGPNLHLDQNT 174

Qy 740 VIOYSWNGLMYFAMGWSRFIWNSRMLYFADLVENEYRMHKSRSYQSCVYMRHLSQEFQ 799
 Db 175 LLQYSWMLFLMA ALGWSYRSQSSANILCFADPLLINEQRMLPCMYDQCKHMLYVSELH 233

Qy 800 WLIQTPDFFLCKMLLFLSTIPVDGLKLNQKFEDLRRNMYKELDRIAKRNPPSCS-R 858
 Db 234 RQVSYEEYLCMKYLLSVPKDGKLSQEFDERMVYKELGAIV KREGLESSONWQ 292

Qy 859 REYQLTKLDSVQPIARELHFTFDLLIKSHMSVDFPEMMAEITSVQPKLTSQVVKVPT 918
 Db 293 RFYQLTKLDSRHEVVENLNQCFQTFDLKTM-SIEFPPEMMAEITNQIYTSNGNIKIL 351

Db 352 LFH 354

RESULT 19

Query Match 19.5%; Score 959.5; DB 6; Length 356;
 Best Local Similarity 52.1%; Pred. No. 3.4e-63;
 Matches 189; Conservative 62; Mismatches 99; Indels 13; Gaps 6;

Qy 563 CLICGDEASGCHYGAATCGSCKVFEKRAEKGQKYLCAASRDCTIDFK 622
 Db 1 CLVCSDEASGCHYGVLTGCSCKVFEKRAEKGQHNYLCAGRNDCTIDKIRRKNCPCRYRK 60

Qy 623 CTEAGMFLGARKLKLQKLNQKQEGEASSSTSPEETTO--KLTVSHTEYECOPITM 679
 Db 61 CLOAGMNLEARTKK-----KIKGQIQTATGVSQETSENPGNKTIVPAPLQLPTPLV 114

Qy 680 VLEAIEPGVYCAGHDNNQNPDSFAALLSSNLFGEROLHVYKWAALPGRNLHYDDQA 739
 Db 115 LLEVTEPEVLTAGTDSVPDSTWRIMTTLNLLGGROVIAAVKWAAPGPNLHLDQNT 174

Qy 740 VIOYSWNGLMYFAMGWSRFIWNSRMLYFADLVENEYRMHKSRSYQSCVYMRHLSQEFQ 799
 Db 175 LLQYSWMLFLMA ALGWSYRSQSSANILCFADPLLINEQRMLPCMYDQCKHMLYVSELH 233

Qy 800 WLIQTPDFFLCKMLLFLSTIPVDGLKLNQKFEDLRRNMYKELDRIAKRNPPSCS-R 858
 Db 234 RQVSYEEYLCMKYLLSVPKDGKLSQEFDERMVYKELGAIV KREGLESSONWQ 292

Qy 859 REYQLTKLDSVQPIARELHFTFDLLIKSHMSVDFPEMMAEITSVQPKLTSQVVKVPT 918
 Db 293 RFYQLTKLDSRHEVVENLNQCFQTFDLKTM-SIEFPPEMMAEITNQIYTSNGNIKIL 351

Db 352 LFH 354

RESULT 20

Query Match 19.5%; Score 959.5; DB 6; Length 356;
 Best Local Similarity 52.1%; Pred. No. 3.4e-63;
 Matches 189; Conservative 62; Mismatches 99; Indels 13; Gaps 6;

Qy 563 CLICGDEASGCHYGAATCGSCKVFEKRAEKGQKYLCAASRDCTIDFK 622
 Db 1 CLVCSDEASGCHYGVLTGCSCKVFEKRAEKGQHNYLCAGRNDCTIDKIRRKNCPCRYRK 60

Qy 623 CTEAGMFLGARKLKLQKLNQKQEGEASSSTSPEETTO--KLTVSHTEYECOPITM 679
 Db 61 CLOAGMNLEARTKK-----KIKGQIQTATGVSQETSENPGNKTIVPAPLQLPTPLV 114

Qy 680 VLEAIEPGVYCAGHDNNQNPDSFAALLSSNLFGEROLHVYKWAALPGRNLHYDDQA 739
 Db 115 LLEVTEPEVLTAGTDSVPDSTWRIMTTLNLLGGROVIAAVKWAAPGPNLHLDQNT 174

Qy 740 VIOYSWNGLMYFAMGWSRFIWNSRMLYFADLVENEYRMHKSRSYQSCVYMRHLSQEFQ 799
 Db 175 LLQYSWMLFLMA ALGWSYRSQSSANILCFADPLLINEQRMLPCMYDQCKHMLYVSELH 233

Qy 800 WLIQTPDFFLCKMLLFLSTIPVDGLKLNQKFEDLRRNMYKELDRIAKRNPPSCS-R 858
 Db 234 RQVSYEEYLCMKYLLSVPKDGKLSQEFDERMVYKELGAIV KREGLESSONWQ 292

Qy 859 REYQLTKLDSVQPIARELHFTFDLLIKSHMSVDFPEMMAEITSVQPKLTSQVVKVPT 918
 Db 293 RFYQLTKLDSRHEVVENLNQCFQTFDLKTM-SIEFPPEMMAEITNQIYTSNGNIKIL 351

Db 352 LFH 354

RESULT 21

Query Match 19.5%; Score 959.5; DB 6; Length 356;
 Best Local Similarity 52.1%; Pred. No. 3.4e-63;
 Matches 189; Conservative 62; Mismatches 99; Indels 13; Gaps 6;

Qy 563 CLICGDEASGCHYGAATCGSCKVFEKRAEKGQKYLCAASRDCTIDFK 622
 Db 1 CLVCSDEASGCHYGVLTGCSCKVFEKRAEKGQHNYLCAGRNDCTIDKIRRKNCPCRYRK 60

Qy 623 CTEAGMFLGARKLKLQKLNQKQEGEASSSTSPEETTO--KLTVSHTEYECOPITM 679
 Db 61 CLOAGMNLEARTKK-----KIKGQIQTATGVSQETSENPGNKTIVPAPLQLPTPLV 114

Qy 680 VLEAIEPGVYCAGHDNNQNPDSFAALLSSNLFGEROLHVYKWAALPGRNLHYDDQA 739
 Db 115 LLEVTEPEVLTAGTDSVPDSTWRIMTTLNLLGGROVIAAVKWAAPGPNLHLDQNT 174

Qy 740 VIOYSWNGLMYFAMGWSRFIWNSRMLYFADLVENEYRMHKSRSYQSCVYMRHLSQEFQ 799
 Db 175 LLQYSWMLFLMA ALGWSYRSQSSANILCFADPLLINEQRMLPCMYDQCKHMLYVSELH 233

Qy 800 WLIQTPDFFLCKMLLFLSTIPVDGLKLNQKFEDLRRNMYKELDRIAKRNPPSCS-R 858
 Db 234 RQVSYEEYLCMKYLLSVPKDGKLSQEFDERMVYKELGAIV KREGLESSONWQ 292

Qy 859 REYQLTKLDSVQPIARELHFTFDLLIKSHMSVDFPEMMAEITSVQPKLTSQVVKVPT 918
 Db 293 RFYQLTKLDSRHEVVENLNQCFQTFDLKTM-SIEFPPEMMAEITNQIYTSNGNIKIL 351

Db 352 LFH 354

RESULT 22

Query Match 19.5%; Score 959.5; DB 6; Length 356;
 Best Local Similarity 52.1%; Pred. No. 3.4e-63;
 Matches 189; Conservative 62; Mismatches 99; Indels 13; Gaps 6;

Qy 563 CLICGDEASGCHYGAATCGSCKVFEKRAEKGQKYLCAASRDCTIDFK 622
 Db 1 CLVCSDEASGCHYGVLTGCSCKVFEKRAEKGQHNYLCAGRNDCTIDKIRRKNCPCRYRK 60

Qy 623 CTEAGMFLGARKLKLQKLNQKQEGEASSSTSPEETTO--KLTVSHTEYECOPITM 679
 Db 61 CLOAGMNLEARTKK-----KIKGQIQTATGVSQETSENPGNKTIVPAPLQLPTPLV 114

Qy 680 VLEAIEPGVYCAGHDNNQNPDSFAALLSSNLFGEROLHVYKWAALPGRNLHYDDQA 739
 Db 115 LLEVTEPEVLTAGTDSVPDSTWRIMTTLNLLGGROVIAAVKWAAPGPNLHLDQNT 174

Qy 740 VIOYSWNGLMYFAMGWSRFIWNSRMLYFADLVENEYRMHKSRSYQSCVYMRHLSQEFQ 799
 Db 175 LLQYSWMLFLMA ALGWSYRSQSSANILCFADPLLINEQRMLPCMYDQCKHMLYVSELH 233

Qy 800 WLIQTPDFFLCKMLLFLSTIPVDGLKLNQKFEDLRRNMYKELDRIAKRNPPSCS-R 858
 Db 234 RQVSYEEYLCMKYLLSVPKDGKLSQEFDERMVYKELGAIV KREGLESSONWQ 292

Qy 859 REYQLTKLDSVQPIARELHFTFDLLIKSHMSVDFPEMMAEITSVQPKLTSQVVKVPT 918
 Db 293 RFYQLTKLDSRHEVVENLNQCFQTFDLKTM-SIEFPPEMMAEITNQIYTSNGNIKIL 351

Db 352 LFH 354

RESULT 23

Query Match 19.5%; Score 959.5; DB 6; Length 356;
 Best Local Similarity 52.1%; Pred. No. 3.4e-63;
 Matches 189; Conservative 62; Mismatches 99; Indels 13; Gaps 6;

Qy 563 CLICGDEASGCHYGAATCGSCKVFEKRAEKGQKYLCAASRDCTIDFK 622
 Db 1 CLVCSDEASGCHYGVLTGCSCKVFEKRAEKGQHNYLCAGRNDCTIDKIRRKNCPCRYRK 60

Qy 623 CTEAGMFLGARKLKLQKLNQKQEGEASSSTSPEETTO--KLTVSHTEYECOPITM 679
 Db 61 CLOAGMNLEARTKK-----KIKGQIQTATGVSQETSENPGNKTIVPAPLQLPTPLV 114

Qy 680 VLEAIEPGVYCAGHDNNQNPDSFAALLSSNLFGEROLHVYKWAALPGRNLHYDDQA 739
 Db 115 LLEVTEPEVLTAGTDSVPDSTWRIMTTLNLLGGROVIAAVKWAAPGPNLHLDQNT 174

Qy 740 VIOYSWNGLMYFAMGWSRFIWNSRMLYFADLVENEYRMHKSRSYQSCVYMRHLSQEFQ 799
 Db 175 LLQYSWMLFLMA ALGWSYRSQSSANILCFADPLLINEQRMLPCMYDQCKHMLYVSELH 233

Qy 800 WLIQTPDFFLCKMLLFLSTIPVDGLKLNQKFEDLRRNMYKELDRIAKRNPPSCS-R 858
 Db 234 RQVSYEEYLCMKYLLSVPKDGKLSQEFDERMVYKELGAIV KREGLESSONWQ 292

Qy 859 REYQLTKLDSVQPIARELHFTFDLLIKSHMSVDFPEMMAEITSVQPKLTSQVVKVPT 918
 Db 293 RFYQLTKLDSRHEVVENLNQCFQTFDLKTM-SIEFPPEMMAEITNQIYTSNGNIKIL 351

Db 352 LFH 354

RESULT 24

Query Match 19.5%; Score 959.5; DB 6; Length 356;
 Best Local Similarity 52.1%; Pred. No. 3.4e-63;
 Matches 189; Conservative 62; Mismatches 99; Indels 13; Gaps 6;

Qy 563 CLICGDEASGCHYGAATCGSCKVFEKRAEKGQKYLCAASRDCTIDFK 622
 Db 1 CLVCSDEASGCHYGVLTGCSCKVFEKRAEKGQHNYLCAGRNDCTIDKIRRKNCPCRYRK 60

Qy 623 CTEAGMFLGARKLKLQKLNQKQEGEASSSTSPEETTO--KLTVSHTEYECOPITM 679
 Db 61 CLOAGMNLEARTKK-----KIKGQIQTATGVSQETSENPGNKTIVPAPLQLPTPLV 114

Qy 680 VLEAIEPGVYCAGHDNNQNPDSFAALLSSNLFGEROLHVYKWAALPGRNLHYDDQA 739
 Db 115 LLEVTEPEVLTAGTDSVPDSTWRIMTTLNLLGGROVIAAVKWAAPGPNLHLDQNT 174

Qy 740 VIOYSWNGLMYFAMGWSRFIWNSRMLYFADLVENEYRMHKSRSYQSCVYMRHLSQEFQ 799
 Db 175 LLQYSWMLFLMA ALGWSYRSQSSANILCFADPLLINEQRMLPCMYDQCKHMLYVSELH 233

Qy 800 WLIQTPDFFLCKMLLFLSTIPVDGLKLNQKFEDLRRNMYKELDRIAKRNPPSCS-R 858
 Db 234 RQVSYEEYLCMKYLLSVPKDGKLSQEFDERMVYKELGAIV KREGLESSONWQ 292

Qy 859 REYQLTKLDSVQPIARELHFTFDLLIKSHMSVDFPEMMAEITSVQPKLTSQVVKVPT 918
 Db 293 RFYQLTKLDSRHEVVENLNQCFQTFDLKTM-SIEFPPEMMAEITNQIYTSNGNIKIL 351

Db 352 LFH 354

RESULT 25

Query Match 19.5%; Score 959.5; DB 6; Length 356;
 Best Local Similarity 52.1%; Pred. No. 3.4e-63;
 Matches 189; Conservative 62; Mismatches 99; Indels 13; Gaps 6;

Qy 563 CLICGDEASGCHYGAATCGSCKVFEKRAEKGQKYLCAASRDCTIDFK 622
 Db 1 CLVCSDEASGCHYGVLTGCSCKVFEKRAEKGQHNYLCAGRNDCTIDKIRRKNCPCRYRK 60

Qy 623 CTEAGMFLGARKLKLQKLNQKQEGEASSSTSPEETTO--KLTVSHTEYECOPITM 679
 Db 61 CLOAGMNLEARTKK-----KIKGQIQTATGVSQETSENPGNKTIVPAPLQLPTPLV 114

Qy 680 VLEAIEPGVYCAGHDNNQNPDSFAALLSSNLFGEROLHVYKWAALPGRNLHYDDQA 739
 Db 115 LLEVTEPEVLTAGTDSVPDSTWRIMTTLNLLGGROVIAAVKWAAPGPNLHLDQNT 174

Qy 740 VIOYSWNGLMYFAMGWSRFIWNSRMLYFADLVENEYRMHKSRSYQSCVYMRHLSQEFQ 799
 Db 175 LLQYSWMLFLMA ALGWSYRSQSSANILCFADPLLINEQRMLPCMYDQCKHMLYVSELH 233

Qy 800 WLIQTPDFFLCKMLLFLSTIPVDGLKLNQKFEDLRRNMYKELDRIAKRNPPSCS-R 858
 Db 234 RQVSYEEYLCMKYLLSVPKDGKLSQEFDERMVYKELGAIV KREGLESSONWQ 292

Qy 859 REYQLTKLDSVQPIARELHFTFDLLIKSHMSVDFPEMMAEITSVQPKLTSQVVKVPT 918
 Db 293 RFYQLTKLDSRHEVVENLNQCFQTFDLKTM-SIEFPPEMMAEITNQIYTSNGNIKIL 351

Db 352 LFH 354

RESULT 26

Query Match 19.5%; Score 959.5; DB 6; Length 356;
 Best Local Similarity 52.1%; Pred. No. 3.4e-63;
 Matches 189; Conservative 62; Mismatches 99; Indels 13; Gaps 6;

Qy 563 CLICGDEASGCHYGAATCGSCKVFEKRAEKGQKYLCAASRDCTIDFK 622
 Db 1 CLVCSDEASGCHYGVLTGCSCKVFEKRAEKGQHNYLCAGRNDCTIDKIRRKNCPCRYRK 60

Qy 623 CTEAGMFLGARKLKLQKLNQKQEGEASSSTSPEETTO--KLTVSHTEYECOPITM 679
 Db 61 CLOAGMNLEARTKK-----KIKGQIQTATGVSQETSENPGNKTIVPAPLQLPTPLV 114

Qy 680 VLEAIEPGVYCAGHDNNQNPDSFAALLSSNLFGEROLHVYKWAALPGRNLHYDDQA 739
 Db 115 LLEVTEPEVLTAGTDSVPDSTWRIMTTLNLLGGROVIAAVKWAAPGPNLHLDQNT 174

Qy 740 VIOYSWNGLMYFAMGWSRFIWNSRMLYFADLVENEYRMHKSRSYQSCVYMRHLSQEFQ 799
 Db 175 LLQYSWMLFLMA ALGWSYRSQSSANILCFADPLLINEQRMLPCMYDQCKHMLYVSELH 233

Qy 800 WLIQTPDFFLCKMLLFLSTIPVDGLKLNQKFEDLRRNMYKELDRIAKRNPPSCS-R 858
 Db 234 RQVSYEEYLCMKYLLSVPKDGKLSQEFDERMVYKELGAIV KREGLESSONWQ 292

Qy 859 REYQLTKLDSVQPIARELHFTFDLLIKSHMSVDFPEMMAEITSVQPKLTSQVVKVPT 918
 Db 293 RFYQLTKLDSRHEVVENLNQCFQTFDLKTM-SIEFPPEMMAEITNQIYTSNGNIKIL 351

Db 352 LFH 354

RESULT 27

Query Match 19.5%; Score 959.5; DB 6; Length 356;
 Best Local Similarity 52.1%; Pred. No. 3.4e-63;
 Matches 189; Conservative 62; Mismatches 99; Indels 13; Gaps 6;

Qy 563 CLICGDEASGCHYGAATCGSCKVFEKRAEKGQKYLCAASRDCTIDFK 622
 Db 1 CLVCSDEASGCHYGVLTGCSCKVFEKRAEKGQHNYLCAGRNDCTIDKIRRKNCPCRYRK 60

Qy 623 CTEAGMFLGARKLKLQKLNQKQEGEASSSTSPEETTO--KLTVSHTEYECOPITM 679
 Db 61 CLOAGMNLEARTKK-----KIKGQIQTATGVSQETSENPGNKTIVPAPLQLPTPLV 114

Qy 680 VLEAIEPGVYCAGHDNNQNPDSFAALLSSNLFGEROLHVYKWAALPGRNLHYDDQA 739
 Db 115 LLEVTEPEVLTAGTDSVPDSTWRIMTTLNLLGGROVIAAVKWAAPGPNLHLDQNT 174

Qy 740 VIOYSWNGLMYFAMGWSRFIWNSRMLYFADLVENEYRMHKSRSYQSCVYMRHLSQEFQ 799
 Db 175 LLQYSWMLFLMA ALGWSYRSQSSANILCFADPLLINEQRMLPCMYDQCKHMLYVSELH 233

Qy 800 WLIQTPDFFLCKMLLFLSTIPVDGLKLNQKFEDLRRNMYKELDRIAKRNPPSCS-R 858
 Db 234 RQVSYEEYLCMKYLLSVPKDGKLSQEFDERMVYKELGAIV KREGLESSONWQ 292

Qy 859 REYQLTKLDSVQPIARELHFTFDLLIKSHMSVDFPEMMAEITSVQPKLTSQVVKVPT 918
 Db 293 RFYQLTKLDSRHEVVENLNQCFQTFDLKTM-SIEFPPEMMAEITNQIYTSNGNIKIL 351

Db 352 LFH 354

RESULT 28

Query Match 19.5%; Score 959.5; DB 6; Length 356;
 Best Local Similarity 52.1%; Pred. No. 3.4e-63;
 Matches 189; Conservative 62; Mismatches 99; Indels 13; Gaps 6;

Qy 563 CLICGDEASGCHYGAATCGSCKVFEKRAEKGQKYLCAASRDCTIDFK 622
 Db 1 CLVCSDEASGCHYGVLTGCSCKVFEKRAEKGQHNYLCAGRNDCTIDKIRRKNCPCRYRK 60

Qy 623 CTEAGMFLGARKLKLQKLNQKQEGEASSSTSPEETTO--KLTVSHTEYECOPITM 679
 Db 61 CLOAGMNLEARTKK-----KIKGQIQTATGVSQETSENPGNKTIVPAPLQLPTPLV 114

Qy 680 VLEAIEPGVYCAGHDNNQNPDSFAALLSSNLFGEROLHVYKWAALPGRNLHYDDQA 739
 Db 115 LLEVTEPEVLTAGTDSVPDSTWRIMTTLNLLGGROVIAAVKWAAPGPNLHLDQNT 174

Qy 740 VIOYSWNGLMYFAMGWSRFIWNSRMLYFADLVENEYRMHKSRSYQSCVYMRHLSQEFQ 799
 Db 175 LLQYSWMLFLMA ALGWSYRSQSSANILCFADPLLINEQRMLPCMYDQCKHMLYVSELH 233

Qy 800 WLIQTPDFFLCKMLLFLSTIPVDGLKLNQKFEDLRRNMYKELDRIAKRNPPSCS-R 858
 Db 234 RQVSYEEYLCMKYLLSVPKDGKLSQEFDERMVYKELGAIV KREGLESSONWQ 292

Qy 859 REYQLTKLDSVQPIARELHFTFDLLIKSHMSVDFPEMMAEITSVQPKLTSQVVKVPT 918
 Db 293 RFYQLTKLDSRHEVVENLNQCFQTFDLKTM-SIEFPPEMMAEITNQIYTSNGNIKIL 351

Db 352 LFH 354

RESULT 29

Query Match 19.5%; Score 959.5; DB 6; Length 356;
 Best Local Similarity 52.1%; Pred. No. 3.4e-63;
 Matches 189; Conservative 62; Mismatches 99; Indels 13; Gaps 6;

Qy 563 CLICGDEASGCHYGAATCGSCKVFEKRAEKGQKYLCAASRDCTIDFK 622
 Db 1 CLVCSDEASGCHYGVLTGCSCKVFEKRAEKGQHNYLCAGRNDCTIDKIRRKNCPCRYRK 60

Qy 623 CTEAGMFLGARKLKLQKLNQKQEGE

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentID® Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/041,886
 FILING DATE: 09-04-2001
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Matthew A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LJ 2626
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
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 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 154 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

-09-041-886-32

Query Match 16.2%; Score 795; DB 4; Le
 Best Local Similarity 95.1%; Fred. No. 1.5e-51;
 Matches 154; Conservative 0; Mismatches 0;

1 MEVQLGLGRYPRPPSKTYRGAQNLFQSREVIQNPGPRHPEAA
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1 MEVQLGLGRYPRPPSKTYRGAQNLFQSREVIQNPGPRHPEAA

61 QQQQQQQQQQQQQQQQQQQQQQQQQQETSPRQQQQGDFGSPQAHRRG
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 58 -----QQQQQQQQQQQQQQQQETSPRQQQQGDFGSPQAHRRG

121 PQSALECHPERGCCVPEPAAVAASGCLPQLPAPDDESSA 16
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 113 PQSALECHPERGCCVPEPAAVAASGCLPQLPAPDDESSA 15

RESULT 14
 -09-041-886-32

Sequence 8, Application US/08875223
 Patent No. 612175

GENERAL INFORMATION:
 APPLICANT: Vigne, Emmanuel
 APPLICANT: PERICAUDDET, Michel
 APPLICANT: DEDIEU, Jean Francois
 APPLICANT: ORSINI, Cecile
 APPLICANT: YEH, Parrice
 APPLICANT: LATTIA, Martine
 APPLICANT: PROST, Edouard

TITLE OF INVENTION: CELLS FOR THE PRODUCTION OF RECOMBINANT ADENOVIRUSES
 NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rhone-Poulenc Rorer Inc.
 STREET: 500 Arcola Road, Mailstop 3C43
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COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentID® Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/875,223
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 95/00747

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31.815
 ; REFERENCE/DOCKET NUMBER: P-UD 1927
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 24:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 284 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-592-214A-24

Query Match 13.18; Score 644; DB 2; Length 284;
 Best Local Similarity 44.48; Pred. No. 4_9e-4;
 Matches 127; Conservative 56; Mismatches 97; Indels 6; Gaps 2;
 QY 636 KIGNLKIQEGEASSTTSPTDETTQKLTVSHIEGECQPTFLNLEATEPGVVCAGHDN 695
 Db 3 KIKKGQDATAVSODSENPKTIVPAALPQL-----TPTLVSLIEVPEVLVAGYDS 57
 QY 656 NQDSEFAALLSSLNELGERQLVHVVWKWAALKPGRNLHVDDQMAVTOYSWNGLMYFAMGW 755
 Db 58 SPEDSAWRIMTILNLGGRTYAAVKWAKAIGLRLNUHLDQMTLQYSWNMLMAFALGW 117
 QY 756 RSFVNNSRMLYFAPDLYVENEYRMHKSRMYSQCVRMRLSOEGHNLQTPOEFLCMKALL 815
 Db 118 RSYRQSSCNLLFAPDLIINEFRMSLPCMDQCKINMLFVSSELQRLOVSYEYLCKMKTLL 177
 QY 816 LFSLIPDGKMKQFFDELRYNIKELDRLTACKRNKNPTSCSRPYQLKLLDSVQPIAR 875
 Db 178 LSSVPKEGLKSQELDEIRMTYIKLGKALVREGNSSONWQRYQLKLLDSMHEVVE 237
 QY 876 EHQFTFDLLKSHMYSVDFPBMMAETISVQPKILSGKTPYFH 921
 Db 238 NULTYCFQTEFLDTM-SIEFFEMLAELITNOIPKYSNGNKKLHF 282

Search completed: January 3, 2002, 23:06:44
 Job time: 5485 sec

